

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: January 3, 2005, 13:53:07 ; Search time 117.153 Seconds  
(without alignments)  
Sequence: 2342.472 Million cell updates/sec

Title: US-09-989-339a-2  
Perfect score: 3905

1 MASHIVGYPRMGPKRKLKFA. .... ALTNMVSATKUJRTOLSAK 765

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext: 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*

1: geneseqp1980s: \*

2: geneseqp1990s: \*

3: geneseqp2000s: \*

4: geneseqp2001s: \*

5: geneseqp2002s: \*

6: geneseqp2003as: \*

7: geneseqp2003bs: \*

8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	3905	100.0	765	Adb23036
2	3697.5	94.7	766	ADA4808
3	3535	90.5	765	ADA3040
4	3502	89.7	6	Adb23045
5	3472	88.9	765	ABR9394
6	3472	88.9	765	ABR9325
7	3467	88.8	765	ADB25084
8	3448	88.3	765	3 ARG53127
9	3448	88.3	765	3 ARG1807
10	3448	88.3	765	5 ABR92196
11	3395	86.9	763	6 ADB23038
12	3394	86.9	755	3 ARG18608
13	3394	86.9	755	3 ARG53128
14	3357.5	86.0	728	6 ADA48334
15	3269.5	83.7	768	ADA48100
16	3215	82.3	717	3 ARG1809
17	3215	82.3	717	3 ARG53129
18	3194.5	81.8	684	6 ADA48126
19	3185	81.6	745	3 ARG27788
20	3131	80.2	735	3 ARG27789
21	3108.5	79.6	807	5 ABR9567
22	2952	75.6	697	3 ARG27790
23	2076	53.2	451	7 ABR73900
24	2050	52.8	446	7 ABR74475
25	2057.5	52.7	474	3 AAG39450

Maximum DB seq length: 0

Minimum DB seq length: 0

#### ALIGNMENTS

26	2003.5	51.3	464	3	AAG39451	Aag39451 Arabidops
27	1833	46.9	758	5	AAU72946	Aau72946 Neisseria
28	1833	46.9	758	5	AAU72999	Aau72999 Neisseria
29	1833	46.9	758	5	AAU72872	Aau72872 Neisseria
30	1824	46.7	758	8	ADP08261	Adp08261 Neisseria
31	1820.5	46.6	426	3	ADP39452	Adp39452 Arabidops
32	1818	46.6	771	6	ABP7516	Abp7516 N. gonorr
33	1776	45.5	768	7	ADP05473	Adf05473 Bacterial
34	1773.5	45.4	794	7	ABO83078	Ab083078 Pseudomon
35	1763	45.1	759	6	ABM68367	Abm68367 Photorhab
36	1757.5	45.0	767	8	ADP99011	Adp99011 C. albica
37	1756.5	45.0	760	7	ABO61538	Ab061538 Klebsiell
38	1714	43.9	765	5	ABB48512	Abb48512 Listeria
39	1694.5	43.4	767	7	ADK63384	Adk63384 Disease t
40	1686	43.2	767	5	ABP65725	Abp65725 Bifidobac
41	1674.5	42.9	759	5	ABBS5491	Abb5491 Lactococc
42	1673	42.8	749	8	ADK46406	Adk46406 Streptococ
43	1663	42.6	745	4	AAG91007	Aag91007 C glutam
44	1663	42.6	745	5	AMM5073	Amm5073 Corynebac
45	1660	42.5	749	6	ABU00960	Abu00960 S. pneumo

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

RESULT	ID	NAME	TYPE	VERSION	DATE	DESCRIPTION
1	ADB23036	ADB23036	standard; protein;	765 AA.	XX	
2	ADB23036;				XX	
3					XX	
4					XX	
5					XX	
6					XX	
7					XX	
8					XX	
9					XX	
10					XX	
11					XX	
12					XX	
13					XX	
14					XX	
15					XX	
16					XX	
17					XX	
18					XX	
19					XX	
20					XX	
21					XX	
22					XX	
23					XX	
24					XX	
25					XX	

**ALIGNMENTS**

New nucleic acid fragments encoding a plant 5-methyltetrahydropteroyl-triglutamate-methyltransferase or methionine synthase, useful for producing increased levels of methionine in the seeds of transformed plant.

Example 1; Fig 2; 69pp; English.

The invention relates to an isolated nucleic acid fragment encoding a plant methionine synthase. The nucleic acid fragments and chimeric genes are useful for producing increased levels of methionine in the seeds of

CC transformed plants. The present sequence represents the amino acid  
 CC sequence of a plant methionine synthase.  
 XX  
 SQ Sequence 765 AA;

XX  
 OS *Oryza sativa*.  
 XX  
 PN WO200300906-A2.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-1B002453.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 PR 26-SEP-2001; 2001US-0352277P.  
 PR 22-MAR-2002; 2002US-0366555P.

XX  
 PA (SYGN ) SYNTENTA PARTICIPATIONS AG.  
 XX  
 PT Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;  
 PI Katagiri F, Krebs J, Provart N, Rieke D, Zhu T;  
 XX  
 DR WPI; 2003-184052/18.  
 DR N-PSDB; ADA48607.

XX  
 PT New polynucleotide comprising a plant nucleotide sequence having an open  
 PT reading frame that encodes a polypeptide associated with disease  
 PT resistance, useful for conferring resistance or tolerance to a plant  
 PT pathogen.  
 XX  
 BS Claim 10; SEQ ID NO 678; 299pp; English.

CC The invention relates to a novel isolated polynucleotide comprising a  
 CC plant nucleotide sequence having an open reading frame that encodes a  
 CC polypeptide associated with disease resistance or its fragment having  
 CC substantially the same activity as the full-length polypeptide. The  
 CC polynucleotide of the invention is useful for conferring resistance or  
 CC tolerance to a plant pathogen. The present sequence represents a protein  
 CC conferring disease resistance used in the invention.  
 XX  
 SQ Sequence 766 AA;

Query Match 94.7%; Score 3697.5; DB 6; Length 766;  
 Matches 716; Conservative 28; Mismatches 21; Indels 1; Gaps 1;

QY 1 MASHIVGPRMGPKRELKFALESFDWGKSSAEDLEKTYATDRISSWIKOMSEAGIKYIFSN 60  
 Db 481 LDIDVLVHGERPERNDMVEYFGEOLSGFAFTANGHMQSYGCSRCKPPIYGDVSRPNPMV 540  
 QY 541 FWWKQNAQMPTRPKGMJTGPPVTLNMSFVRNDOPRETYCQALAIKEVDELEAGIQ 600  
 Db 541 FWKQNAQMPTRPKGMJTGPPVTLNMSFVRNDOPRETYCQALAIKEVDELEAGIQ 600  
 QY 601 VIQIDEALREGPLRKSEHAFYLDWAVHSRFTNCQVQDTPQHTMCYNSNDIHSI 660  
 Db 601 VIQIDEALREGPLRKSEHAFYLDWAVHSRFTNCQVQDTPQHTMCYNSNDIHSI 660  
 QY 661 IDMDADVITIENRSDEKLISVREGVKGAGIGPGVWIDHSRIPSTEIBADVERKMLA 720  
 Db 661 IDMDADVITIENRSDEKLISVREGVKGAGIGPGVWIDHSRIPSTEIBADVERKMLA 720  
 QY 721 VFDTNLWNPNPDGKTRKTYEKPLTMVMSKLTQLSAK 765  
 Db 721 VFDTNLWNPNPDGKTRKTYEKPLTMVMSKLTQLSAK 765

RESULT 2

ADA48608 ID ADA48608 standard; protein; 766 AA.

AC ADA48608;

XX DT 20-NOV-2003 (first entry)

XX DB Rice protein conferring disease resistance in plants.

KW disease resistance; pathogen tolerance; plant pathogen; plant; rice.

XX  
 OS *Oryza sativa*.  
 XX  
 PN WO200300906-A2.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002WO-1B002453.  
 XX  
 PR 22-JUN-2001; 2001US-0300112P.  
 PR 26-SEP-2001; 2001US-0352277P.  
 PR 22-MAR-2002; 2002US-0366555P.

XX  
 PA (SYGN ) SYNTENTA PARTICIPATIONS AG.  
 XX  
 PT Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;  
 PI Katagiri F, Krebs J, Provart N, Rieke D, Zhu T;  
 XX  
 DR WPI; 2003-184052/18.  
 DR N-PSDB; ADA48607.

XX  
 PT New polynucleotide comprising a plant nucleotide sequence having an open  
 PT reading frame that encodes a polypeptide associated with disease  
 PT resistance, useful for conferring resistance or tolerance to a plant  
 PT pathogen.  
 XX  
 BS Claim 10; SEQ ID NO 678; 299pp; English.

CC The invention relates to a novel isolated polynucleotide comprising a  
 CC plant nucleotide sequence having an open reading frame that encodes a  
 CC polypeptide associated with disease resistance or its fragment having  
 CC substantially the same activity as the full-length polypeptide. The  
 CC polynucleotide of the invention is useful for conferring resistance or  
 CC tolerance to a plant pathogen. The present sequence represents a protein  
 CC conferring disease resistance used in the invention.  
 XX  
 SQ Sequence 766 AA;

Query Match 94.7%; Score 3697.5; DB 6; Length 766;  
 Matches 716; Conservative 28; Mismatches 21; Indels 1; Gaps 1;

QY 1 MASHIVGPRMGPKRELKFALESFDWGKSSAEDLEKTYATDRISSWIKOMSEAGIKYIFSN 60  
 Db 1 MASHIVGPRMGPKRELKFALESFDWGKSSAEDLEKTYATDRISSWIKOMSEAGIKYIFSN 60  
 QY 61 TSSYDQDFTTAMLGAVERPSWTGGBIGLSTYFSMARGNATVPAFEMTKWDFDTNHFPI 120  
 Db 61 TSSYDQDFTTAMLGAVERPSWTGGBIGLSTYFSMARGNATVPAFEMTKWDFDTNHFPI 120  
 QY 121 VPELGPSPKFTVASHKAVSEYKAKALGIDTVPLVGVPSVYLLSKPKGVKVSFSISSL 180  
 Db 121 VPELGPSPKFTVASHKAVSEYKAKALGIDTVPLVGVPSVYLLSKPKGVKVSFSISSL 180  
 QY 181 LOSILIPKTYEVAELKAGATWQFDEPTLVLDLDSHQAFAFSAYTELESALISGLWLI 240  
 Db 181 LOSILIPKTYEVAELKAGATWQFDEPTLVLDLDSHQAFAFSAYTELESALISGLWLI 240  
 QY 241 ETYFADPAESYKLTLSVSGVYAGFDLIRGAKTDLIKSAGFPGSKYLFAGVUDGRNII 300  
 Db 241 ETYFADPAESYKLTLSVSGVYAGFDLIRGAKTDLIKSAGFPGSKYLFAGVUDGRNII 300  
 QY 300 ADDLAASITSLHSLEAVGKDKLUVSTCSLMTAVDLVNETKUDDEIKSFLAFAOKV 359  
 Db 301 ADDLAASITSLHSLEAVGKDKLUVSTCSLMTAVDLVNETKUDDEIKSFLAFAOKV 360  
 QY 360 EVNALAKALAGQDEYVFAANAAQASRRSSPRTNEEVOKAAALRGSDHERSTVSLA 419  
 Db 361 EVNALAKALAGQDEYVFAANAAQASRRSSPRTNEEVOKAAALRGSDHERSTVSLA 420  
 QY 420 LDAQQKKUNLPVLIPTTIGSFQTVELRVRREYKACKTDEYISAIKEEIKVQK 479  
 Db 421 LDAQQKKUNLPVLIPTTIGSFQTVELRVRREYKACKTDEYISAIKEEIKVQK 480

SQ	Sequence 765 AA;
Query Match	90.5%; Score 3535; DB 6; Length 765;
Best Local Similarity	88.5%; Pred. No. 2e-287; Matches 677; Conservative 38; Mismatches 50; Indels 0; Gaps 0;
Matches	677; Conservative 38; Mismatches 50; Indels 0; Gaps 0;
1	MASHIVGYPYRPGPKRBLKFALESFDGKSAEDEKVLATDLSSTWKSQNSBAGKIVIPSN 60
1	MASHIVGYPYRPGPKRBLKFALESFDGKSAEDEKVLATDLSSTWKSQNSBAGKIVIPSN 60
QY	61 TSYYDQVLDTTAMIGAVPVERYSWYGIGLSTYFSMARGNATPAMENTKWFDTNHYPI 120
Db	61 TFSYDQVLDTTAMIGAVPVERYSWYGIGLSTYFSMARGNATPAMENTKWFDTNHYPI 120
QY	121 VPELGPSKTYTAYASHKAVASPKYEAKGADTPTVPLVGPVSYLISKPKGCKVECPSSL 180
Db	121 VPELGPSKTYTAYASHKAVASPKYEAKGADTPTVPLVGPVSYLISKPKGCKVECPSSL 180
QY	181 LGSLIPIKYKEVVAELKAGASWIQDPEIWKDQDAHLEAFASSAYELESSFGNLNVL 240
Db	181 LDKVLPYKEVIAEKGASWIQDPEIWKDQDAHLEAFASSAYELESSFGNLNVL 240
QY	241 ETYFADIPARPSYKULTSLCUTAYGFDLIRGAKTDLINSSPSGSKYFLAGVWGRNTWA 300
Db	241 ETYFADIPARPSYKULTSLCUTAYGFDLIRGAKTDLINSSPSGSKYFLAGVWGRNTWA 300
QY	301 DDLANSLSTLHSLEAVAGKDLVUSTSCLMHTAVDNLVNETKLDDEIKSKLAFAQKVE 360
Db	301 NDLAASINLILQSLEBGIVKGOKLUVSTCSILHTAVDNLVNETKLDDEIKSKLAFAQKVE 360
QY	361 VNALAKALAGQKDEVYFAANAAQASRSSPRVTNEVOKAALRGSDHRSSTVSLR 420
Db	361 VNALAKALAGKDEAFFSANTAQASRSSPRVTNEVOKAALRGSDHRSSTVSLR 420
QY	421 DAQKQLNLVPLPTTIGSPOTVBLRVRREYKAKKTFDEYISAKEBISKVVKQEE 480
Db	421 DAQKQLNLVPLPTTIGSPOTVBLRVRREYKAKKTFDEYISAKEBISKVVKQEE 480
QY	481 LDIDIVLHGPERNDMVEYFGEOQLSGFAFFTANGWQYQSGRCVKEPPIYGDVSRNPMTV 540
Db	481 LDIDIVLHGPERNDMVEYFGEOQLSGFAFFTANGWQYQSGRCVKEPPIYGDVSRNPMTV 540
QY	541 FWSKMAQSMPRPKGMLTCPVTLINASVNRNDOPRFECYQIALAIKEVEDLEAGI 600
Db	541 FWSKMAQSMPRPKGMLTCPVTLINASVNRNDOPRFECYQIALAIKEVEDLEAGI 600
QY	601 VQIDEAALREGPLPKRSHAFYDWAIVSFRINTVQGVDTTQIHTHMCYNSFNDIHSI 660
Db	601 VQIDEAALREGPLPKRSHAFYDWAIVSFRINTVQGVDTTQIHTHMCYNSFNDIHSI 660
QY	661 IDMDADVITIENSRSDEKULSVFREGVKGAGIGPVGVDIHSPRIPSTEIADREVKMLA 720
Db	661 IDMDADVITIENSRSDEKULSVFREGVKGAGIGPVGVDIHSPRIPSTEIADREVKMLA 720
QY	721 VFDNILWNPDCGKTRKTYEVPALENNVSAKIRIOLASSK 765
Db	721 VFDNILWNPDCGKTRKTYEVPALENNVSAKIRIOLASSK 765
RESULT 3	
ID	ADB23040 standard; protein; 765 AA.
XX	
AC	ADB23040;
XX	
DT	20-NOV-2003 (first entry)
XX	
DB	Tobacco methionine synthase.
XX	
KW	enzyme; plant; methionine synthase; methionine; seed; transformed plant;
XX	
OS	Nicotiana tabacum.
XX	
US	US2003098886-A1.
XX	
PR	08-MAY-2003.
XX	
PR	28-JAN-2002; 2002US-00989339.
XX	
PR	30-AUG-1995; 95US-0002973P.
PR	27-AUG-1996; 96US-00703829.
PR	19-AUG-1999; 99US-00377431.
XX	
PA	(FALC/) FALCO S. C.
PA	(FAMO/) RAMODU O. O.
PA	(RAFA/) RAFALSKI J. A.
PA	(RAMA/) RAMAKER M. L.
PA	(TARC/) TARCZYNSKI M. C.
PA	(THOR/) THORPE C.
XX	
PI	Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarzynski MC;
XX	
PI	Thorpe C;
DR	WPI; 2003-657990/62.
DR	N-PSDB; ADB23039.
XX	
PT	New nucleic acid fragments encoding a plant 5-methyltetrahydropteroyl-triglutamate-homocysteine methyl transferase or methionine synthase, useful for producing increased levels of methionine in the seeds of transformed plants. The present sequence represents the amino acid sequence of a plant methionine synthase.
XX	
PS	Example 1; Fig 2; 69pp; English.
RESULT 4	
ID	ADB23045
XX	
AC	ADB23045;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Madagascar periwinkle methionine synthase.
XX	
AC	
XX	
PS	
CC	The invention relates to an isolated nucleic acid fragment encoding a plant methionine synthase. The nucleic acid fragments and chimeric genes are useful for producing increased levels of methionine in the seeds of transformed plants. The present sequence represents the amino acid sequence of a plant methionine synthase.
CC	

XX US2003088886-A1.  
 PN 08-MAY-2003.  
 PD XX 28-JAN-2002; 2002US-00989339.  
 PR XX 30-AUG-1995; 95US-0002973P.  
 PR 27-AUG-1995; 96US-00703829.  
 PR XX 19-AUG-1999; 99US-00377431.  
 PR XX (FALC/) FALCO S C.  
 PA (FAMO/) FAMODU O O.  
 PA (RAFA/) RAFALSKI J A.  
 PA (RAMA/) RAMAKER M L.  
 PA (TARC/) TARCZYNSKI M C.  
 PA XX (THOR/) THORPE C.  
 PI Falco SC, Famodu OO, Rafalski JA, Ramaker ML, Tarczyński MC;  
 XX PI Thorpe C;  
 XX DR WPI; 2003-657990/62.

XX PT New nucleic acid fragments encoding a plant 5-methyltetrahydropteroyltriglutamate-homocysteine methyl transferase or methionine synthase, useful for producing increased levels of methionine in the seeds of transformed plants.

XX PS Example 1; Fig 2; 69pp; English.

CC The invention relates to an isolated nucleic acid fragment encoding a plant methionine synthase. The nucleic acid fragments and chimeric genes are useful for producing increased levels of methionine in the seeds of transformed plants. The present sequence represents the amino acid sequence of a plant methionine synthase.

XX SQ Sequence 765 AA;

Query Match 89.7%; Score 3502; DB 6; Length 765;  
 Best Local Similarity 87.5%; Pred. No. 1.2e-284;  
 Matches 669; Conservative 47; Mismatches 49; Indels 0; Gaps 0;

CC 1 MASHIVGIPRMGPKRELKFALPSFWDGKGSADPLERKATDLSSSIWOMSEAGIKYIPSN 60  
 1 MASHIVGIPRMGPKRELKFALPSFWDKSSAELDOKYIADLSSSIWOMADAGIKYIPSN 60

CC 61 TSSYDPOQDTTMLGAVPERSWTGCIGLISYPSMARGNATVPAKEMTKPDTNHF 120  
 61 TFSYDPOQDTTMLGAVPERSWTGCIGLISYPSMARGNATVPAKEMTKPDTNHF 120

DB 121 VPLGPSTKFTASHKAVSEYKEAKALGIDTWTVLGVPSVYIILSKPAKGVRSFSLISL 180  
 121 VPLGPSTKFTASHKAVSEYKEAKALGIDTWTVLGVPSVYIILSKPAKGVRSFSLISL 180

CC 181 LQSLIPITKEVAKELKAGASWQDLDPELTLQDADAEHLAASSAYABLESSPFSGLNLT 240  
 181 LQKLPVKEVIGELKAGASWQDPETLVLDLSEHOLEAFKAYSBLESTLGLNIV 240

CC 241 ETYFADIPAESTKTLTSLSGVAVGFDLIRGKTLDRSSPSGKYLFGAGVTDGRNIA 300  
 241 ETYFADIPAESTKTLTSLSGVAVGFDLIRGKTLDRSSPSGKYLFGAGVTDGRNIA 300

DB 301 DDLASISLTHSLPEAVAGDKDQKVSTSGLMMHTAVDVLNETKLDDETKSWLAAQKVE 360  
 301 DDLASISLTHSLPEAVAGDKDQKVSTSGLMMHTAVDVLNETKLDDETKSWLAAQKVE 360

CC 361 VNALAKALAGQDQEYFANAAQASRSRSPRVNEEYOKAAALRGSDHRSTTVSRL 420  
 361 VNALAKALAGQDQEYFANAAQASRSRSPRVNEEYOKAAALRGSDHRSTTVSRL 420

CC 421 DAQOKKLNLPVLTGTSFPTVVELVRVREYKAKITEDSYISAIKEIKWVQI 480  
 421 DAQOKKLNLPVLTGTSFPTVVELVRVREYKAKITEDSYISAIKEIKWVQI 480

CC 421 DAQOKKLNLPVLTGTSFPTVVELVRVREYKAKITEDSYISAIKEIKWVQI 480

XX SQ Sequence 765 AA;

Query Match 88.9%; Score 3472; DB 5; Length 765;  
 Best Local Similarity 86.8%; Pred. No. 3.8e-282;  
 Matches 664; Conservative 47; Mismatches 54; Indels 0; Gaps 0;

CC 541 FWSKMAQSMTPRPMKGMLTGPTILNWFSVRNDQPRFETCQIAIAKIKKEYDELEAGIQ 600  
 541 FWSQTAQSMTPRPMKGMLTGPTILNWFSVRNDQPRFETCQIAIAKIKKEYDELEAGIQ 600

DB 601 VQIDEALARESPLRSEHAYLDWAWHSRITNGQVQDPTQIHTMCYENFDLHSI 660  
 601 VQIDEALARESPLRSEHAYLDWAWHSRITNGQVQDPTQIHTMCYENFDLHSI 660

DB 601 VQIDEALARESPLRSEHAYLDWAWHSRITNGQVQDPTQIHTMCYENFDLHSI 660

DB 661 IDMDADTTIENSRSKLLS/FREGVYKAGIGPGYDHSRIPSTEEADRINMLA 720  
 661 IDMDADTTIENSRSKLLS/FREGVYKAGIGPGYDHSRIPSTEEADRINMLA 720

CC 721 VFTDTNLLWNPDCGLKTRKYTEVKPAIINMVSATKLTQLASAK 765  
 721 VFTDTNLLWNPDCGLKTRKYTEVKPAIENMVSAAKLTQLASAK 765

XX SQ Sequence 765 AA;

RESULT 5  
 ID ABB93994  
 ID ABB93994 standard; protein; 765 AA.  
 ID ABB93994;  
 XX DT 31-MAY-2002 (first entry)  
 XX DE Herbicidally active polypeptide SEQ ID NO 3205.  
 XX KW Herbicidal; plant; agriculture; herbicide.  
 XX OS Arabidopsis thaliana.  
 XX PN WO200210210-A2.  
 XX PD 07-FEB-2002.  
 XX PR 28-AUG-2001; 2001WO-EP009892.  
 XX PR (FARB ) BAYER AG.  
 XX PT Tietjen K, Weidler M;  
 XX DR WPI; 2002-269010/31.  
 XX PT Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.  
 XX PS Claim 5; SEQ ID NO 3205; 261pp + Sequence Listing; English.  
 XX CC The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides

CC SQ Sequence 765 AA;

Query Match 88.9%; Score 3472; DB 5; Length 765;  
 Best Local Similarity 86.8%; Pred. No. 3.8e-282;  
 Matches 664; Conservative 47; Mismatches 54; Indels 0; Gaps 0;

PR	28-AUG-2001; 2001WO-EP009892.
Db	1 MASHIVGYPRMGPKRELKFALESFDWKGSSADELEYKATDRSSWQKOMSEAGIKIYPSN 60
Db	1 MASHIVGYPRMGPKRELKFALESFDWKGSSADELEYKATDRSSWQKOMSAAGTKFIPSN 60
Db	61 TSSYDQVLDTTAMGAVPERYSWTFGEIGLSTYFMSMARGNATVAPMENWKWFDTNHYI 120
Db	121 VPELGPSTKFTYASHKAVSEYKEAKALGIDTYPVPGPVSYLLSKPAGKVEKSFSLSL 180
Db	61 TFAHYDQVLDTTAMGAVPERYGEIGLDTYFMSMARGNATVAPMENWKWFDTNHYI 120
Qy	181 LGSIPIKYKVAEKAAGASWIQDDEPTLVKDLDAHAFSSAYELESSFGSLNVL 240
Db	181 LPKIPLIPIKVEVTEKAAGATWQDPEVPLVMDLGQKLOAFTGAYAELBLSTLGLNVL 240
Db	241 ETYFADIPASYSKFTLTSQGTYAFDGLRGAKTDLIRSSPSPSKYLFAGVVDGRNTWA 300
Db	241 ETYFADIPASYSKFTLTSQGTYAFDGLRGAKTDLIRSSPSPSKYLFAGVVDGRNTWA 300
Qy	301 DDLASLSTLHSLEAVAGKDLVWSTCSLMHATDVLVNEWTKLDEIKSMLAFAAQVUE 360
Db	301 NDFAASLSTLQALEGFTVGDOKLKVWTSCLSLHTAVDLINETKLDEIKSMLAFAAQVUE 360
Qy	361 VNALLAKALAGQKDETYFAANAAQASRSRSPRVTIEVQAAALRGSDHRSRTSVSRL 420
Db	361 VNALLAKALAGQKDEALFSANAAALRSRSPRVTIEVQAAALKGSDHRSRTSVSRL 420
Qy	421 DAQQKLNIPVPLPTTIGSFQPTVLRVVEREYKAKKTEDEYISAIKEISKVKIOB 480
Db	421 DAQQKLNIPVPLPTTIGSFQPTVLRVVEREYKAKKTEDEYISAIKEISKVKIOB 480
Qy	481 LDIDVLVHGERPERNDMVEYFGEOLSGFAFTANGWQSYGSRCVCKPPIYGDVSRPKAMTV 540
Db	481 LDIDVLVHGERPERNDMVEYFGEOLSGFAFTANGWQSYGSRCVCKPPIYGDVSRPKAMTV 540
Qy	541 FWSKNAQSMTPRPMGMLTGPTVTLNWSFTRNDQDRPFTQYQIAAIKEVEDIEAGIQ 600
Db	541 FWSKNAQSMTPRPMGMLTGPTVTLNWSFTRNDQDRPFTQYQIAAIKEVEDIEAGIQ 600
Qy	601 VQIDEALREGPLRKSEHAFYDWAHSFRITCGVQDPTQIHTHMCYNSNDIHSI 660
Db	601 VQIDEALREGPLRKSEHAFYDWAHSFRITCGVQDPTQIHTHMCYNSNDIHSI 660
Qy	661 IDMDPDTIENSRSDEKLSVFRGGVKGAGIGPGVYDHSPRIPSSERIADRNKMLA 720
Db	661 IDMDPDTIENSRSDEKLSVFRGGVKGAGIGPGVYDHSPRIPSSERIADRNKMLA 720
Qy	721 VFDTNTLWNPDCGKTRKTEVPLTNNVSATKURQOLASAK 765
Db	721 VLEQNLWNPDCGKTRKTEVPLTNNVSATKURQOLASAK 765
RESULT 6	
ABR93525	ABR93525 standard; protein: 765 AA.
AC	ABR93525;
XX	31-MAY-2002 (first entry)
XX	Herbicidally active polypeptide SEQ ID NO 2736.
XX	Herbicidal; plant; agriculture; herbicide.
XX	Arabidopsis thaliana.
XX	WO200210210-A2.
XX	07-FEB-2002.
XX	28-AUG-2001; 2001WO-EP009892.
Qy	1 MASHIVGYPRMGPKRELKFALESFDWKGSSADELEYKATDRSSWQKOMSEAGIKIYPSN 60
Qy	1 MASHIVGYPRMGPKRELKFALESFDWKGSSADELEYKATDRSSWQKOMSAAGTKFIPSN 60
Qy	121 VPELGPSTKFTYASHKAVSEYKEAKALGIDTYPVPGPVSYLLSKPAGKVEKSFSLSL 180
Qy	61 TFAHYDQVLDTTAMGAVPERYGEIGLDTYFMSMARGNATVAPMENWKWFDTNHYI 120
Qy	181 LGSIPIKYKVAEKAAGASWIQDDEPTLVKDLDAHAFSSAYELESSFGSLNVL 240
Qy	181 LPKIPLIPIKVEVTEKAAGATWQDPEVPLVMDLGQKLOAFTGAYAELBLSTLGLNVL 240
Qy	241 ETYFADIPASYSKFTLTSQGTYAFDGLRGAKTDLIRSSPSPSKYLFAGVVDGRNTWA 300
Qy	301 DDLASLSTLHSLEAVAGKDLVWSTCSLMHATDVLVNEWTKLDEIKSMLAFAAQVUE 360
Qy	361 VNALLAKALAGQKDEALFSANAAALRSRSPRVTIEVQAAALKGSDHRSRTSVSRL 420
Qy	421 DAQQKLNIPVPLPTTIGSFQPTVLRVVEREYKAKKTEDEYISAIKEISKVKIOB 480
Qy	481 LDIDVLVHGERPERNDMVEYFGEOLSGFAFTANGWQSYGSRCVCKPPIYGDVSRPKAMTV 540
Qy	541 FWSKNAQSMTPRPMGMLTGPTVTLNWSFTRNDQDRPFTQYQIAAIKEVEDIEAGIQ 600
Qy	541 FWSKNAQSMTPRPMGMLTGPTVTLNWSFTRNDQDRPFTQYQIAAIKEVEDIEAGIQ 600
Qy	601 VQIDEALREGPLRKSEHAFYDWAHSFRITCGVQDPTQIHTHMCYNSNDIHSI 660

QY	661	IDMDADVITIENSRSDEKLUISVFRGKVKGAGIGGVYDTHSPRPSTEADREVKMLA	720	601 VIQIDBAALREGPLRPLRSKHEAFYLDWAVHSFRITNCGVQDSTQIHTM	660
Db	661	IDMDADVITIENSRSDEKLUISVFRGKVKGAGIGGVYDTHSPRPSTEADREVKMLA	720	61 TPAHYDQVLDTAMLGAVPRKGTYGEGIGDVFMSHGNASVPAHE	660
QY	721	VFDTNILWNPDCGKTRKYTEVKALTNMSATKLRTQIASK	765	121 VFLGLGSTKFTYASHKAVSBYKEAKLGIDTVPLVGPVSYLILSKP	660
Db	721	VLEONILWNPDCGKTRKYTEVKALNOMVDAAKLIRSOLASAK	765	121 VFLGPVNFSYASHKAVSBYKEAKLGIDTVPLVGPVSYLILSKP	660
QY	RESULT 7			181 LGSILPQYKEVVAELKAGASWQLEBPTVQDHAELAFLASSAYE	660
ID	ADE25084	standard; protein; 765 AA.		181 LPKILPQYKEVITELKAGATWIOLEPVLVMDLEGKQLOAFTGAYA	660
AC	ADE25084:			241 ETYFADIPAEASYKTLTSLSGVTAAGFDLIRGAKTLDIIRSPPSGKVL	660
XX				241 ETYFADIPAEASYKTLTSLSGVTAAGFDLIRGAKTLDIIRSPPSGKVL	660
DT	29-JAN-2004	(first entry)		301 DDLASLSTLISLEAVAGKDKLWSTCSLMTAVDVLVNETKLDDEK	660
DE	Plant growth associated protein seq id 59.			301 NDAASLSTLQALEBGTGKDKLWSTCSLMTAVDVLVNETKLDDEK	660
XX	plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis; Brassica; Zea; Oryza; Triticum; Hordeum; Loliu			361 VNALAKALAGQKDEVFPANAAQASRRSSPRVNEEVQAKAALRGSS	660
KW	Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon; Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus; Quercus.			361 VNALAKALAGQKDEVFPANAAQASRRSSPRVNEEVQAKAALRGSS	660
OS	Magnoliophyta.			421 DAQOKKUNLPLPILPTTGSFPOTVELRVRREYKAKVSEEDYVKA	660
XX	US2003188343-A1.			421 DAQOKKUNLPLPILPTTGSFPOTVELRVRREYKAKVSEEDYVKA	660
PN				481 LDIDVLVHGEPERNDMVEYFGRBOLSGRAFTANGWVOSYGRCKPRTI	660
XX	PD 02-OCT-2003.			481 LDIDVLVHGEPERNDMVEYFGRBOLSGRAFTANGWVOSYGRCKPRTI	660
PF	07-JAN-2003; 2003US-00338777.			541 FWSKMAOSMTPPMKGMLTGPTILNWSFVRNDQPRETCQIALATR	660
XX	PR 09-JAN-2002; 2002US-0347288P.			541 FWSKMAOSMTPPMKGMLTGPTILNWSFVRNDQPRETCQIALATR	660
DR	N-PSDB; ADE25054.			601 VIQIDEALREGPLRKSSEAHYLDWAVHSFRITNCGVQDSTQIHTM	660
XX	PA (LINK-) LINK THERAPEUTICS INC.			601 VIQIDEALREGPLRKSSEAHYLDWAVHSFRITNCGVQDSTQIHTM	660
PI	Bowen BA, Haudenschild CD, Buckler ES;			601 VIQIDEALREGPLRKSSEAHYLDWAVHSFRITNCGVQDSTQIHTM	660
XX	WPT; 2003-803305/75.			661 IDMDADVITIENSRSDEKLUISVFRGKVKGAGIGGVYDTHSPRPSTEADREVKMLA	660
DR	N-PSDB; ADE25054.			661 IDMDADVITIENSRSDEKLUISVFRGKVKGAGIGGVYDTHSPRPSTEADREVKMLA	660
XX	PT New isolated or recombinant polypeptide for use in modulating a plant growth trait in a flowering plant e.g. in <i>Arabidopsis</i> , <i>Brassica</i> , <i>Zea</i> , or <i>Oryza</i> .			721 VFDTNILWNPDCGKTRKYTEVKALTNMSATKLRTQIASK	660
PT	PT New isolated or recombinant polypeptide for use in modulating a plant growth trait in a flowering plant e.g. in <i>Arabidopsis</i> , <i>Brassica</i> , <i>Zea</i> , or <i>Oryza</i> .			721 VLEONILWNPDCGKTRKYTEVKALNOMVDAAKLIRSOLASAK	660
XX	PS Claim 8; SEQ ID NO 59; 81PP; English.			721 VLEONILWNPDCGKTRKYTEVKALNOMVDAAKLIRSOLASAK	660
CC	The invention describes an isolated or recombinant polypeptide (I) comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in the specification, or a conservative variant; (b) encoded by 1 of 30 sequences (S2), as given in the specification, or a conservative variant; (c) encoded by a sequence that hybridises under stringent conditions to sequence (S2); and (d) encoded by a sequence 70 % identical to S2. The expression or activity of (I) is modulated to modulate a plant growth trait in a flowering plant, of the family Brassicaceae, preferably in a plant that is <i>Arabidopsis</i> , <i>Brassica</i> , <i>Zea</i> , <i>Oryza</i> , <i>Triticum</i> , <i>Hordeum</i> , <i>Loliu</i> , <i>Sorghum</i> , <i>Capsicum</i> , <i>Gossypium</i> , <i>Hevea</i> , <i>Beta</i> , <i>Vitis</i> , <i>Solanum</i> , <i>Lycopersicon</i> , <i>Capsicum</i> , <i>Gossypium</i> , <i>Hevea</i> , <i>Linum</i> , <i>Prunus</i> , <i>Citrus</i> , <i>Populus</i> , <i>Pinus</i> , or <i>Quercus</i> . A new method is used to detect genes for a plant growth trait. This is the amino acid sequence of plant growth associated protein.			QY 61 TSYYDOVLDTAMLGAVPERSWTGBEGIGSTYFSMGINATVPMEE	660
CC	Sequence 765 AA;			61 TSYYDOVLDTAMLGAVPERSWTGBEGIGSTYFSMGINATVPMEE	660
CC	Best local Similarity 86.7%; Pred. No. 1e-281; Indels 0; Gaps 0;			61 TSYYDOVLDTAMLGAVPERSWTGBEGIGSTYFSMGINATVPMEE	660
CC	Matches 663; Conservative 47; Mismatches 55;			61 TSYYDOVLDTAMLGAVPERSWTGBEGIGSTYFSMGINATVPMEE	660
QY	1 MASHIVGPRMGPKEKLFALESFWGKQSSAEDLKVATDLRSSWQMSAGIKYKIPSN	60		61 TSYYDOVLDTAMLGAVPERSWTGBEGIGSTYFSMGINATVPMEE	660

PR	25-FEB-1999;	990US-0121825P.	PR	13-JUL-1999;	990US-0143542P.
PR	05-MAR-1999;	990US-0123180P.	PR	14-JUL-1999;	990US-0143624P.
PR	09-MAR-1999;	990US-0123548P.	PR	15-JUL-1999;	990US-0144005P.
PR	13-MAR-1999;	990US-0125788P.	PR	16-JUL-1999;	990US-014485P.
PR	25-MAR-1999;	990US-0126264P.	PR	16-JUL-1999;	990US-0144086P.
PR	29-MAR-1999;	990US-0126785P.	PR	19-JUL-1999;	990US-0144325P.
PR	01-APR-1999;	990US-0127462P.	PR	19-JUL-1999;	990US-0144331P.
PR	06-APR-1999;	990US-0128234P.	PR	19-JUL-1999;	990US-0144332P.
PR	07-APR-1999;	990US-0128714P.	PR	19-JUL-1999;	990US-0144333P.
PR	16-APR-1999;	990US-0128845P.	PR	19-JUL-1999;	990US-0144334P.
PR	19-APR-1999;	990US-0130077P.	PR	19-JUL-1999;	990US-0144335P.
PR	21-APR-1999;	990US-0130449P.	PR	20-JUL-1999;	990US-0144352P.
PR	23-APR-1999;	990US-0130891P.	PR	20-JUL-1999;	990US-0144632P.
PR	28-APR-1999;	990US-0131449P.	PR	20-JUL-1999;	990US-0144884P.
PR	08-APR-1999;	990US-013204.	PR	21-JUL-1999;	990US-0144814P.
PR	30-APR-1999;	990US-0132407P.	PR	21-JUL-1999;	990US-014506P.
PR	04-MAY-1999;	990US-0132484P.	PR	22-JUL-1999;	990US-0145088P.
PR	05-MAY-1999;	990US-0132485P.	PR	22-JUL-1999;	990US-0145087P.
PR	06-MAY-1999;	990US-0132486P.	PR	22-JUL-1999;	990US-0145089P.
PR	07-MAY-1999;	990US-0132863P.	PR	23-JUL-1999;	990US-0145145P.
PR	11-MAY-1999;	990US-0134256P.	PR	23-JUL-1999;	990US-0145218P.
PR	14-MAY-1999;	990US-0134218P.	PR	23-JUL-1999;	990US-0145224P.
PR	14-MAY-1999;	990US-0134219P.	PR	26-JUL-1999;	990US-0145276P.
PR	14-MAY-1999;	990US-0134221P.	PR	27-JUL-1999;	990US-0145913P.
PR	14-MAY-1999;	990US-0134370P.	PR	27-JUL-1999;	990US-0145918P.
PR	19-MAY-1999;	990US-0134765P.	PR	27-JUL-1999;	990US-0145919P.
PR	20-MAY-1999;	990US-0134941P.	PR	28-JUL-1999;	990US-0145951P.
PR	21-MAY-1999;	990US-0134949P.	PR	02-AUG-1999;	990US-0146386P.
PR	24-MAY-1999;	990US-0135535P.	PR	02-AUG-1999;	990US-0146388P.
PR	25-MAY-1999;	990US-0135629P.	PR	02-AUG-1999;	990US-0147303P.
PR	07-JUN-1999;	990US-0136021P.	PR	03-AUG-1999;	990US-0147308P.
PR	07-JUN-1999;	990US-013632P.	PR	04-AUG-1999;	990US-0147309P.
PR	10-JUN-1999;	990US-0136782P.	PR	04-AUG-1999;	990US-0147302P.
PR	10-JUN-1999;	990US-0137222P.	PR	05-AUG-1999;	990US-0147192P.
PR	03-JUN-1999;	990US-0137528P.	PR	05-AUG-1999;	990US-0147260P.
PR	04-JUN-1999;	990US-0137502P.	PR	06-AUG-1999;	990US-0147303P.
PR	07-JUN-1999;	990US-0137724P.	PR	06-AUG-1999;	990US-0147416P.
PR	08-JUN-1999;	990US-0138094P.	PR	09-AUG-1999;	990US-0147430P.
PR	10-JUN-1999;	990US-0138540P.	PR	04-AUG-1999;	990US-0147935P.
PR	01-JUN-1999;	990US-0138847P.	PR	10-AUG-1999;	990US-0148171P.
PR	14-JUN-1999;	990US-0139119P.	PR	11-AUG-1999;	990US-0148319P.
PR	16-JUN-1999;	990US-0139452P.	PR	12-AUG-1999;	990US-0148341P.
PR	17-JUN-1999;	990US-0139453P.	PR	13-AUG-1999;	990US-0148565P.
PR	18-JUN-1999;	990US-0139492P.	PR	13-AUG-1999;	990US-014864P.
PR	18-JUN-1999;	990US-0139460P.	PR	16-AUG-1999;	990US-0149368P.
PR	18-JUN-1999;	990US-0139455P.	PR	17-AUG-1999;	990US-0149175P.
PR	18-JUN-1999;	990US-0139462P.	PR	18-AUG-1999;	990US-0149426P.
PR	18-JUN-1999;	990US-0139457P.	PR	20-AUG-1999;	990US-0149722P.
PR	18-JUN-1999;	990US-0139458P.	PR	20-AUG-1999;	990US-0149723P.
PR	18-JUN-1999;	990US-0139763P.	PR	20-AUG-1999;	990US-0149929P.
PR	21-JUN-1999;	990US-0139817P.	PR	23-AUG-1999;	990US-0149902P.
PR	22-JUN-1999;	990US-0139899P.	PR	23-AUG-1999;	990US-0149930P.
PR	23-JUN-1999;	990US-0140353P.	PR	25-AUG-1999;	990US-0150566P.
PR	23-JUN-1999;	990US-0140354P.	PR	26-AUG-1999;	990US-0150884P.
PR	24-JUN-1999;	990US-0140695P.	PR	27-AUG-1999;	990US-0151065P.
PR	06-JUL-1999;	990US-0142390P.	PR	27-AUG-1999;	990US-0151066P.
PR	08-JUL-1999;	990US-012803P.	PR	27-AUG-1999;	990US-0151080P.
PR	09-JUL-1999;	990US-0142920P.	PR	30-AUG-1999;	990US-0151303P.
PR	12-JUL-1999;	990US-0142977P.	PR	31-AUG-1999;	990US-0151438P.
PR	01-JUL-1999;	990US-0142154P.	PR	01-SEP-1999;	990US-0151930P.
PR	02-JUL-1999;	990US-0142055P.	PR	07-SEP-1999;	990US-0152363P.
PR	06-JUL-1999;	990US-0142390P.	PR	10-SEP-1999;	990US-0153070P.
PR	19-JUL-1999;	990US-0142877P.	PR	13-SEP-1999;	990US-0153758P.
PR	21-JUL-1999;	990US-0142877P.	PR	15-SEP-1999;	990US-0154018P.
PR	23-JUL-1999;	990US-0142877P.	PR	16-SEP-1999;	990US-0154039P.
PR	02-SEP-1999;	990US-0154779P.	PR	01-SEP-1999;	990US-0151930P.
PR	22-SEP-1999;	990US-0155139P.	PR	23-SEP-1999;	990US-0155486P.
PR	24-SEP-1999;	990US-0155659P.	PR	24-SEP-1999;	990US-0155659P.
PR	28-SEP-1999;	990US-0156458P.	PR	29-SEP-1999;	990US-0156596P.

PR	04-OCT-1999;	990US-0157117P.
PR	05-OCT-1999;	990US-0157753P.
PR	06-OCT-1999;	990US-0157865P.
PR	07-OCT-1999;	990US-0158029P.
PR	08-OCT-1999;	990US-0158232P.
PR	12-OCT-1999;	990US-0158369P.
PR	13-OCT-1999;	990US-0159293P.
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PR	13-OCT-1999;	990US-0159295P.
PR	14-OCT-1999;	990US-0159329P.
PR	14-OCT-1999;	990US-0159330P.
PR	14-OCT-1999;	990US-0159331P.
PR	14-OCT-1999;	990US-0159637P.
PR	14-OCT-1999;	990US-0159638P.
PR	18-OCT-1999;	990US-0159584P.
PR	21-OCT-1999;	990US-0160741P.
PR	21-OCT-1999;	990US-0160767P.
PR	21-OCT-1999;	990US-0160768P.
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PR	21-OCT-1999;	990US-0160814P.
PR	21-OCT-1999;	990US-0160815P.
PR	22-OCT-1999;	990US-0160980P.
PR	22-OCT-1999;	990US-0160981P.
PR	22-OCT-1999;	990US-0160989P.
PR	25-OCT-1999;	990US-0161404P.
PR	25-OCT-1999;	990US-0161405P.
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PR	26-OCT-1999;	990US-0161359P.
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PR	26-OCT-1999;	990US-0161361P.
PR	28-OCT-1999;	990US-0161920P.
PR	29-OCT-1999;	990US-0162142P.
Query Match		
Best Local Similarity	88.3%	Score 3448; DB 3; Length 765;
Matches	661;	Conservative 46; Mi matches 58; Index 0; Gaps 0;
QY	1 MASHIVGVPRMGPGRKELPKALESFWDGKGSAADEKVKATDILRSSTIWKOMSEAGTKVIPSN 60	XX
Db	1 MASHIVGVPRMGPGRKELPKALESFWDGKGSADDLQKVADLRSIWKQMSAGKXKIPSN 60	PR
QY	61 TSSYDQVADTTAMGAVBERYSWGTGGEGILSTYFERSMARGNATPAMEMTKWFDTNYHFI 120	PR
Db	61 TFSHVQDVADTTAMGAVFERSRIGTSGEILQDVFVFSMARGNATPAMEMTKWFDTNYHFI 120	PR
QY	121 VPELGPGSTKPTYASHKAVSYKEAKALGIDTVPUWGVPSYLUISKPKAKGVKEKRSLLSL 180	PR
Db	121 VPELGPVEKSYASHKAVSYKEAKALGVETVPUWGVPSYLUISKPKAKGVKEKRSLLSL 180	PR
QY	181 LGSLIPPIKVEVVAEIKAGASWIQDDEPTVKDQDHAELAFASSYAEJESSFCSGLNVL 240	PR
Db	181 LPKPLIPVYKEVIAEIKAGASWIQDDEPLFVMDLEGHKQLOAFSCAYAEESTLGLNVL 240	PR
QY	241 ETYPADIPAPSYKUTSISGQVATGQDPLRGAKTUDLTSFPGSKYLFAGVWQDNTWA 300	PR
Db	241 ETYPADIPAPAKYTKITSLKQVATGQDPLRGAKTUDLTSFPGSKYLFAGVWQDNTWA 300	PR
QY	301 DDIASLSTHSLEAVAGDKLKVSTSCSLMHTAVDLYMNETKLDDEIKSLAFAAQKVE 360	PR
Db	301 NDIAASLSTHSLEAVAGDKLKVSTSCSLMHTAVDLYMNETKLDDEIKSLAFAAQKVE 360	PR
QY	361 VNALAKALAGQOKDWFYANAAQOSRSRSPRVTNEVOKAAMLRGSDRRTSFTVSARL 420	PR
Db	361 VDALAKALAGQTNESFFTANADALSSRSRSPRVTNEVOKAAMLRGSDRRTSFTVSARL 420	PR
QY	421 DAQOKKLNPILPVTITGSPPTQVLLRREYKAKKTTDEYVISAIKEBSIKVKI03E 480	PR
Db	421 DAQOKKLNPILPVTITGSPPTQVLLRREYKAKKTTDEYVISAIKEBSIKVKI03E 480	PR
QY	481 LDIDVLVHGERPERMDVMEYFGEQLSGPAFTANGWQSYGSRCVKEPIVGDVSPRNPMTV 540	PR
RESULT 9		
ID	AAG18607	standard; protein; 765 AA.
XX	AAG18607;	
AC		
XX		
DT	17-OCT-2000	(first entry)
XX		
DE	Arapidopsis thaliana	protein fragment SEQ ID NO: 20084.
XX		
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PP	25-FEB-2000; 2000EP-00301439.	
XX		
PR	25-FEB-1999; 990US-0121825P.	
PR	05-MAR-1999; 990US-0121818P.	
PR	09-MAR-1999; 990US-0123548P.	
PR	23-MAR-1999; 990US-0125788P.	
PR	25-MAR-1999; 990US-0126264P.	
PR	29-MAR-1999; 990US-0126785P.	
PR	01-APR-1999; 990US-0127462P.	
PR	06-APR-1999; 990US-0128234P.	
PR	08-APR-1999; 990US-0128714P.	
PR	16-APR-1999; 990US-0128845P.	
PR	19-APR-1999; 990US-0130077P.	
PR	21-APR-1999; 990US-0130449P.	
PR	23-APR-1999; 990US-0130510P.	
PR	23-APR-1999; 990US-0130891P.	
PR	28-APR-1999; 990US-0134449P.	
PR	30-APR-1999; 990US-0132048P.	
PR	30-APR-1999; 990US-013256P.	
PR	04-MAY-1999; 990US-0134848P.	
PR	05-MAY-1999; 990US-012485P.	
PR	06-MAY-1999; 990US-013486P.	
PR	06-MAY-1999; 990US-013487P.	
PR	07-MAY-1999; 990US-0132863P.	
PR	11-MAY-1999; 990US-013256P.	
PR	14-MAY-1999; 990US-0134218P.	
PR	14-MAY-1999; 990US-0134219P.	
PR	14-MAY-1999; 990US-0134221P.	
PR	14-MAY-1999; 990US-0134470P.	
PR	19-MAY-1999; 990US-0134768P.	
PR	20-MAY-1999; 990US-0135124P.	
PR	21-MAY-1999; 990US-0135353P.	
PR	24-MAY-1999; 990US-0136229P.	

PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0147038P.
PR	27-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
PR	28-MAY-1999;	99US-0136782P.	PR	04-AUG-1999;	99US-0147302P.
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Query Match 88.3%; Score 3448; DB 3; Length 765;  
Best Local Similarity 86.4%; Pred. No. 4e-280; Mismatches 58; Indels 0; Gaps 0;  
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1 MASHIVGPRMGPKRELKFALESFWDGKSSADDLQKVSDIWKOMSAAGIKYIPSN 60

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61 TFSHYDQVDTTAMLGAVPSPRSYRGFTSGEIGLSTYFSMARGNATPAMENTKWFDTNHYI 120

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QY 181 LGSILPTIYKEVVAELKAAGASWTOLEDEPTLVKOLDAHELAATSSAYAELERSFSGLNVL 240  
181 LPKLPVYKEVIAELKAAGASWTOLEDEPLFVMDLEGHKLQASGAYAELERSFSGLNVL 240

QY 241 ETYFADIPAESEYKLTLSGVTAVGFDLIRGAKTLDLIRSSFPSGKVLFAGVVDGRNIWA 300  
241 ETYFADIPAEYKLTLSGVTAVGFDLIRGAKTLDLIRSSFPSGKVLFAGVVDGRNIWA 300

Db 301 DDLASLSTLHSLEAVAGDKLWVSTSSSLMTAVDNLNETKLDEEIKSWLAAQKVE 360  
301 DDLASLSTLHSLEAVAGDKLWVSTSSSLMTAVDNLNETKLDEEIKSWLAAQKVE 360

QY 361 VNALAKALAGQDEVYFAANAAQASRSRSPRTNEVQKAALRGSDRSTTVA 420  
361 VNALAKALAGQDEVYFAANAAQASRSRSPRTNEVQKAALRGSDRSTTVA 420

Db 421 DAQKKKMLIPVLPPTTISFSPQTELRRVREYKAKITTEDEVTSIAKEIKVVKTORE 480  
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QY 481 LDIDVLUVGEPERNDMVEYFGBOLSGFAFTANGWVOSYGSRCVKPPIYGDYSPRNPMTV 540  
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Db 601 VIQIDEALREGPLRKESBHAFLDWAHVSFRTRNCGVQDTQIHTMCYNSNDIHSI 660  
601 VIQIDEALREGPLRKESBHAFLDWAHVSFRTRNCGVQDTQIHTMCYNSNDIHSI 660

QY 661 IDMDADVITIENSDEKLSVREGVYGAIGPQVWDIHSRPRIPSTEADVERKMLA 720  
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Db 721 VFTPNILMWNPDCGLKTRKTYTEVKPALKMVAKLRSQLSGAK 765  
721 VFTPNILMWNPDCGLKTRKTYTEVKPALKMVAKLRSQLSGAK 765

QY 721 VFTPNILMWNPDCGLKTRKTYTEVKPALKMVAKLRSQLSGAK 765  
721 VFTPNILMWNPDCGLKTRKTYTEVKPALKMVAKLRSQLSGAK 765

RESULT 10

ABB92196 ID ABB92196 standard; protein; 765 AA.  
XX AC ABB92196;  
XX DT 31-MAY-2002 (first entry)  
XX DE Herbicidally active polypeptide SEQ ID NO 1407.  
XX KW Herbicidal; plant; agriculture; herbicide.  
XX OS Arabidopsis thaliana.

XX PN WO200210210-A2.  
XX PD 07-FEB-2002.  
XX PR 28-AUG-2001; 2001WO-EP009892.  
XX PA (FARB ) BAYER AG.  
XX PI Tretjen K, Weidler M;  
XX DR WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.

XX PS Claim 5; SEQ ID NO 1407; 261PP + Sequence Listing; English.

CC The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using a greater search parameter, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides

CC herbicides

XX Sequence 765 AA;

Query Match 88.3%; Score 3448; DB 5; Length 765;  
Best Local Similarity 86.4%; Pred. No. 4e-280; Mismatches 58; Indels 0; Gaps 0;  
Matches 661; Conservative 46; MisMatches 58; Indels 0; Gaps 0;

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121 VPELGPSTKFTYASHKAVSEYKEAKALGIDTPVLUFGVSYLLSKPAKGVRFSFLSL 180  
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QY 181 LGSILPTIYKEVVAELKAAGASWTOLEDEPTLVKOLDAHELAATSSAYAELERSFSGLNVL 240  
181 LPKLPVYKEVIAELKAAGASWTOLEDEPLFVMDLEGHKLQASGAYAELERSFSGLNVL 240

QY 301 DDLASLSTLHSLEAVAGDKLWVSTSSSLMTAVDNLNETKLDEEIKSWLAAQKVE 360  
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QY 361 VNALAKALAGQDEVYFAANAAQASRSRSPRTNEVQKAALRGSDRSTTVA 420  
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Db 420 DAQKKKMLIPVLPPTTISFSPQTELRRVREYKAKITTEDEVTSIAKEIKVVKTORE 480  
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QY 481 LDIDVLUVGEPERNDMVEYFGBOLSGFAFTANGWVOSYGSRCVKPPIYGDYSPRNPMTV 540  
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Db 481 LDIDVLUVGEPERNDMVEYFGBOLSGFAFTANGWVOSYGSRCVKPPIYGDYSPRNPMTV 540



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PR	29-SEP-1999;	990US-01566458P.
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PR	05-OCT-1999;	990US-0157753P.
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Query	Match	86.9%; Score 3394; DB 3; Length 755;
Best	Local Similarity	86.2%; Pred. No. 1.3e-275;
Matches	651; Conservative	46; Mismatches
	58; Index	0; Gaps
		0; Gaps
QY	11	MGPKRERLKPALESFWDGKSAEDEKRYVATDLRSSIWQMSBAGIKYIPTSNWSSYDQVLQD 70
Db	1	MGPKRERLKPALESFWDGKSAEDEKRYVATDLRSSIWQMSBAGIKYIPTSNWSSYDQVLQD 60
QY	71	TTMMLGAVPERYSTGEGLSTYFSSMARGNATVAMENTKWPDTNYHFVPELGPSTK P 130
Db	61	TTMMLGAVPSRYGFTSGEIGLUDVYFSSMARGNASHVAMENTKWPDTNYHYFVPELGPSTK P 120
QY	131	TWASHKAYSEKEAKALGIDTVPUVNGPVSYLLSKPKAGKVEKSISSLSLGSISIPIKE 190
Db	121	SYASHKAYNEKEAKALGIVTVPVLPVGPSYLLSKPLAKGVDKSPDLSLSPKIPKIVKE 180
QY	191	VVABLKAGAGSWIOLDEPTLVKQDIAHELJAFSSYAELOSSFSGIANVILLETYPADTPE 250
Db	181	VIAELKAGAGSWIOLDEPLFVMDLIEGHKQJQFGSGAYAELSTLSGIANVILTYFADTPE 240
QY	251	SYKTLTSLSGVTAYGFDLIRGAKDULDLISSPPSKYFLAGWVDRNITWADDLASSLTL 310
Db	241	AYKNTLTSLSGVTAYGFDLIRGAKDULDLISSPPSKYFLAGWVDRNITWADDLASSLTL 300
QY	311	HSLEAVAGDKLWVSTSCSLMHTAVDLVNEETKLDDEIKSMLAFAAQKVVEVNAALKALAG 370
Db	301	QSLEGWVGDKLWVSTSCSLIHTAVDLINETKLDDEIKSMLAFAAQKVVEVDAALKALAG 360
QY	371	QKOBVYFVANAAQASRSRSRPRVNEEVOKAAMLRGSDRRTSVSARIDAQOKKLNL P 430
Db	361	QTNESSFTANADALSSRSRSRPRVNEEVOKAAMLRGSDRRTSVSARIDAQOKKLNL P 420
431	VLPTTIGSFSPOTVELRRTREYKIKKITEDEYIISAIKEISKVVKIOEFLDIDVHGE 490	
Db	421	ILPTTIGSFSPOTVELRRTREYKAKKISEBEDYVKA 491
QY		PERNDMVEYFGEQLSGFAFRANGWQYQSGRSCKVPLP.
Db	481	PERNDMVEYFGEQLSGFAFTANGWQYQSGRSCKVPLP.
QY	551	PRPMKGMLTGCPVTLNWSTVRNDQPRFETCYQIAI
Db	541	KRPKGMLTGCPVTLNWSTVRNDQPRFETCYQIAI
QY	611	EGPLRKSRHAFYLDWAVSPRITNGVQDPTTOITH
Db	601	EGPLRKSRHAFYLDWAVSPRITNGVQDPTTOITH
QY	671	ENRSDEKULSVFREGVKYQAGIGPGVYDHSPIRPS
Db	661	ENRSDEKULSVFREGVKYQAGIGPGVYDHSPIRPS
QY	731	PDCGKTRKTEVTPALTTNWSATKLIRQOLASAK 7
Db	721	PDCGKTRKTEVTPALTTNWSATKLIRQOLASAK 7
RESULT	13	
PR	AG53128	
ID	AG53128	standard; protein; 755 AA.
XX	XX	
AC	AG53128;	
XX	XX	
DT	18-OCT-2000	(first entry)
XX	XX	
DE	Arabidopsis thaliana protein fragment	SEQ ID N
XX	Protein identification; signal transduction pa	
KW	hybridisation assay; genetic mapping; gene exp	
KW	termination sequence.	
XX	OS	
Arabidopsis thaliana.		
XX		
PN		
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000;	2000EP-00301439.
XX		
PR	05-MAR-1999;	990US-0121825P.
PR	09-MAR-1999;	990US-0123180P.
PR	23-MAR-1999;	990US-0125788P.
PR	25-MAR-1999;	990US-0126264P.
PR	29-MAR-1999;	990US-0126785P.
PR	01-APR-1999;	990US-0127462P.
PR	06-APR-1999;	990US-0128234P.
PR	08-APR-1999;	990US-0128714P.
PR	16-APR-1999;	990US-0129845P.
PR	19-APR-1999;	990US-0130077P.
PR	21-APR-1999;	990US-0130498P.
PR	23-APR-1999;	990US-0130510P.
PR	23-APR-1999;	990US-0130891P.
PR	28-APR-1999;	990US-0131449P.
PR	30-APR-1999;	990US-0132048P.
PR	30-APR-1999;	990US-0132407P.
PR	04-MAY-1999;	990US-0132484P.
PR	05-MAY-1999;	990US-0132485P.
PR	06-MAY-1999;	990US-0132486P.
PR	06-MAY-1999;	990US-0132487P.
PR	07-MAY-1999;	990US-0132863P.
PR	11-MAY-1999;	990US-0134256P.
PR	14-MAY-1999;	990US-0134258P.
PR	14-MAY-1999;	990US-0134259P.
PR	14-MAY-1999;	990US-0134221P.
PR	14-MAY-1999;	990US-0134221P.
PR	18-MAY-1999;	990US-0134768P.

PR	19-MAY-1999;	99US-0134941P.	PR	28-JUL-1999;	99US-014551P.
PR	20-MAY-1999;	99US-013514P.	PR	02-AUG-1999;	99US-0146386P.
PR	21-MAY-1999;	99US-013533P.	PR	02-AUG-1999;	99US-0146388P.
PR	24-MAY-1999;	99US-0135629P.	PR	02-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0147038P.
PR	27-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
PR	28-MAY-1999;	99US-0136782P.	PR	04-AUG-1999;	99US-0147302P.
PR	30-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0147322P.
PR	03-JUN-1999;	99US-0137520P.	PR	05-AUG-1999;	99US-0147320P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-014716P.
PR	08-JUN-1999;	99US-0138094P.	PR	09-AUG-1999;	99US-0147433P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147335P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	99US-0139119P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139432P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-014855P.
PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-0148884P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139466P.	PR	18-AUG-1999;	99US-0149466P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	99US-0139459P.	PR	20-AUG-1999;	99US-0149959P.
PR	18-JUN-1999;	99US-0139460P.	PR	23-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149330P.
PR	18-JUN-1999;	99US-0139462P.	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	99US-0139753P.	PR	27-AUG-1999;	99US-0151070P.
PR	21-JUN-1999;	99US-0139817P.	PR	27-AUG-1999;	99US-0153758P.
PR	22-JUN-1999;	99US-0139899P.	PR	30-AUG-1999;	99US-015130P.
PR	01-JUL-1999;	99US-0141842P.	PR	31-AUG-1999;	99US-0151438P.
PR	01-JUL-1999;	99US-0140333P.	PR	01-SEP-1999;	99US-0151530P.
PR	23-JUN-1999;	99US-0140349P.	PR	20-SEP-1999;	99US-0151779P.
PR	24-JUN-1999;	99US-0140655P.	PR	22-SEP-1999;	99US-0152163P.
PR	24-JUN-1999;	99US-0140823P.	PR	23-SEP-1999;	99US-0153070P.
PR	06-JUL-1999;	99US-0142390P.	PR	10-SEP-1999;	99US-0153070P.
PR	08-JUL-1999;	99US-0142803P.	PR	13-SEP-1999;	99US-0153758P.
PR	09-JUL-1999;	99US-0142920P.	PR	15-SEP-1999;	99US-0154018P.
PR	12-JUL-1999;	99US-0142977P.	PR	16-SEP-1999;	99US-0154039P.
PR	13-JUL-1999;	99US-0143542P.	PR	20-SEP-1999;	99US-0154779P.
PR	01-JUL-1999;	99US-0142154P.	PR	26-AUG-1999;	99US-0155139P.
PR	02-JUL-1999;	99US-0142055P.	PR	07-SEP-1999;	99US-0152163P.
PR	06-JUL-1999;	99US-0142390P.	PR	27-AUG-1999;	99US-0151066P.
PR	22-JUN-1999;	99US-0140991P.	PR	27-AUG-1999;	99US-0149959P.
PR	22-JUN-1999;	99US-0139899P.	PR	30-AUG-1999;	99US-0149330P.
PR	01-JUL-1999;	99US-0141842P.	PR	31-AUG-1999;	99US-0150566P.
PR	23-JUN-1999;	99US-0140333P.	PR	01-SEP-1999;	99US-0151530P.
PR	24-JUN-1999;	99US-0140349P.	PR	20-SEP-1999;	99US-0151779P.
PR	24-JUN-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-0152163P.
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0153070P.
PR	08-JUL-1999;	99US-0142803P.	PR	13-SEP-1999;	99US-0153758P.
PR	12-JUL-1999;	99US-0142920P.	PR	15-SEP-1999;	99US-0154018P.
PR	13-JUL-1999;	99US-0143542P.	PR	16-SEP-1999;	99US-0154039P.
PR	14-JUL-1999;	99US-0143624P.	PR	20-SEP-1999;	99US-0154779P.
PR	15-JUL-1999;	99US-0144055P.	PR	26-AUG-1999;	99US-0155139P.
PR	16-JUL-1999;	99US-0144055P.	PR	05-OCT-1999;	99US-0157753P.
PR	16-JUL-1999;	99US-0144056P.	PR	06-OCT-1999;	99US-0157865P.
PR	19-JUL-1999;	99US-0144335P.	PR	24-SEP-1999;	99US-0155659P.
PR	19-JUL-1999;	99US-0144335P.	PR	28-SEP-1999;	99US-0156458P.
PR	20-JUL-1999;	99US-0144325P.	PR	29-SEP-1999;	99US-0156596P.
PR	20-JUL-1999;	99US-0144433P.	PR	04-OCT-1999;	99US-0157717P.
PR	19-JUL-1999;	99US-0144332P.	PR	22-SEP-1999;	99US-0152163P.
PR	19-JUL-1999;	99US-0144332P.	PR	23-SEP-1999;	99US-0153070P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144332P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159332P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159332P.
PR	20-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-01444632P.	PR	14-OCT-1999;	99US-0159638P.
PR	20-JUL-1999;	99US-01444632P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144884P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0144884P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	22-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145224P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145224P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145276P.	PR	21-OCT-1999;	99US-0160814P.
PR	27-JUL-1999;	99US-0145913P.	PR	21-OCT-1999;	99US-0160815P.
PR	27-JUL-1999;	99US-0145913P.	PR	22-OCT-1999;	99US-016080P.
PR	27-JUL-1999;	99US-0145918P.	PR	22-OCT-1999;	99US-0160818P.
PR	27-JUL-1999;	99US-0145918P.	PR	22-OCT-1999;	99US-0160989P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161040P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161045P.
PR	27-JUL-1999;	99US-0145918P.	PR	26-OCT-1999;	99US-0161359P.

PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR OCT-1999; 99US-0161992P.  
 PR 28-OCT-1999; 99US-0161993P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match 86.9%; Score 3394; DB 3; Length 755;  
 Best Local Similarity 86.2%; Pred. No. 1.3e-275;  
 Matches 651; Conservative 46; Mismatches 58; Indels 0; Gaps 0;

QY 11 MGPKRBLKFALESFDNGKSSSEDELEKATDPRRSSTWIKOMSEAGIKYIPSNNSYYKQD  
 1 MGPKRBLKFALESFDNGKSSADLQKVSADRLRSIDWIKOMSHAGIKYIPSNFTSHYDQVL  
 71 TAMILGAVPERYSWTOGEIGSTYPSMARGNATPAMENTKWFDTNHFVPELGPSTKF  
 61 TTAMIGAVPERYSWTOGEIGSTYPSMARGNATPAMENTKWFDTNHFVPELGPSTKF  
 QY 131 TYASHKAVSEYKEAKALGIDTVPLVGPVSYLLSKPAKGKPSLSSLHSIPIYKE 70  
 121 SYASHKAVSEYKEAKALGIVETVPLVGPVSYLLSKPAKGKPSLSSLHSIPIYKE 60  
 Db 191 VWAELKAAGASWIQDDEPTVNDLQHAEFLAFASSAYAELSSFSGNVNLJTYFADIP  
 181 VIAELKAAGASWIQDLEPFLVMDLQHLOQFSGAYAELSTLGLNVLVLYTYFADIP 120  
 251 SYKTLTSLSGYTAYGEDLIRGAKTDLIRSSSSPGSKYLFGAVVGDGRNIMADLAASTL  
 241 AKYTTLSKQVTAQFDPDVLGKTKDPLKSGFPOCKYLFAGVGDGRNIMADLAASTL 310  
 Db 311 HSLEAVAGKOKLKVSTSCSLMHTAVDVLNETKLDDBIKSWAFAAQKVUNVALAKALAG  
 301 OSLEGVVGKOKLKVSTSCSLHATDVLNETKLDDBIKSWAFAAQKVUNVALAKALAG 370  
 QY 371 QKDETYFAAAMQAQSRSSPRVTEBEVQAAARGSRDIRSTRSTVSARADQAQKTNLP  
 361 QTNESPFATANDAJSRRSSPRVTEBSVOKAALKGSDHRRTEVSARLDAQOKQNL 430  
 Db 431 VLPPTTIGSPPQTVELRVRVRBVKAKKITEDEYISAIKEISKVVKIQEIDLIVHGE  
 421 ILPTTITGSFPTVLSRVRVREYKAKKISDEYVKAIEKKVVDIQEIDLIVHGE 490  
 QY 491 PERNDWVEYGGEOQSGPAFTANGWQSYGRCVKUPIYEDVSRDNPMTVFWSKMAQSM  
 481 PERNDWVEYGGEOQSGPAFTANGWQSYGRCVKUPVXGDSRFPKMTVFWSSQAQSM 550  
 QY 551 PRPMKGMLTGPTVTLNWSFVRNDOPRHETCYQIAAIKEVEDLKGIGVQIDEAAR  
 541 KRPKGMLTGPTVTLNWSFVRNDOPRHETCYQIAAIKEVEDLKGIGVQIDEAAR 600  
 Db 611 EGLPLRKSEHAFYLDWAVSRFTRITGQVDTQIHTHMCYCSNFNDIHSIDMDADVT  
 601 EGLPLRKSEHAFYLDWAVSRFTRITGQVDTQIHTHMCYCSNFNDIHSIDMDADVT 670  
 QY 601 EGLPLRKSEHAFYLDWAVSRFTRITGQVDTQIHTHMCYCSNFNDIHSIDMDADVT 660  
 Db 61 TPSYDQVDTTAMGAVPERYSWTOGEIGSTYPSMARGNATPAMENTKWFDTNHF  
 QY 61 TPSYDQVDTTAMGAVPERYSWTOGEIGSTYPSMARGNATPAMENTKWFDTNHF 120  
 Db 121 VPELGPSTKPTYASHKAVSEYKEAKALGIDTVPLVGPVSYLLSKPAKGKPSLSSL  
 121 VPELGPNTKPSYSSHAKAVSEYKEAKALGIDTVPLVGPVSYLLSKPAKGKPSLSSL 180  
 QY 181 LGSLTPYKEVWAKAGASWIQDDEPTVNDLQHAEFLAFASSAYAELSSFSGNVNL  
 661 ENSRSEDEKULSVFREGVKYKGIGPGVYDHSRIPSTDIBADRINKMLAVLQNILWN 720  
 QY 731 PDCGKTRKTYTEVKALTNMSATKLIRQOLASAK 765  
 Db 721 PDCGLKTRKTYTEVKPALKAMVDAKUQLRSQLSAK 755

RESULT 14

ADA48634 ID ADA48634 Standard; protein; 728 AA.  
 XX AC ADA48634;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Rice protein conferring disease resistance in plants.

QY 300 ADDLAASSTLHSLEAVAGKDKLKVSTSCSLMHTAVDVLNETKLDDETSKSWAFAAQKV 359  
 301 ADDLAASSTLHSLEAVOKDKLKVSTSCSLMHTAVDVLNETKLDSEKSWAFAAQKV 360  
 QY 360 EVNALAKALAGAQKDE-----VFAAMAAQSRSSPRVTEBEVQAA 402  
 Db 361 EVNALAKALAGAQKDEHKLKULLITYFVNINIVQYFAAMAAQSRSSPRVTEBEVQAA 420  
 QY 403 AALGSDHRRSTVSARLDAQQKLNLPVLPPTTIGSPPQTVELRVRREYKAKKITEDE 462

XX disease resistance; pathogen tolerance; plant pathogen; plant; rice.  
 KW  
 XX OS Oryza sativa.  
 XX PN WO200300905-A2.  
 XX PD 03-JAN-2003.  
 XX PF 21-JUN-2002; 2002WO-IB002453.  
 XX PR 22-JUN-2001; 2001US-0300112P.  
 PR 26-SEP-2001; 2001US-0352277P.  
 PR 22-MAR-2002; 2002US-0366535P.  
 XX FA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX PI Glazebrook, J., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.;  
 Katagiri, F., Kreps, J., Provart, N., Riecke, D., Zhu, T.;  
 XX WPI: 2003-184052/18.  
 DR N-PSDB; ADA48633.

XX PT New polynucleotide comprising a plant nucleotide sequence having an open  
 PT reading frame that encodes a polypeptide associated with disease  
 PT resistance, useful for conferring resistance or tolerance to a plant  
 PT pathogen.

XX PS Claim 10; SEQ ID NO 704; 299pp; English.

XX The invention relates to a novel isolated polynucleotide comprising a  
 CC plant nucleotide sequence having an open reading frame that encodes a  
 CC polypeptide associated with disease resistance or its fragment having  
 substantially the same activity as the full-length polypeptide. The  
 CC polynucleotide of the invention is useful for conferring resistance or  
 CC tolerance to a plant pathogen. The present sequence represents a protein  
 CC conferring disease resistance used in the invention.

XX Sequence 728 AA;

QY 491 PERNDWVEYGGEOQSGPAFTANGWQSYGRCVKUPIYEDVSRDNPMTVFWSKMAQSM 550  
 481 PERNDWVEYGGEOQSGPAFTANGWQSYGRCVKUPVXGDSRFPKMTVFWSSQAQSM 540  
 QY 551 PRPMKGMLTGPTVTLNWSFVRNDOPRHETCYQIAAIKEVEDLKGIGVQIDEAAR 600  
 541 KRPKGMLTGPTVTLNWSFVRNDOPRHETCYQIAAIKEVEDLKGIGVQIDEAAR 600  
 Db 611 EGLPLRKSEHAFYLDWAVSRFTRITGQVDTQIHTHMCYCSNFNDIHSIDMDADVT 670  
 601 EGLPLRKSEHAFYLDWAVSRFTRITGQVDTQIHTHMCYCSNFNDIHSIDMDADVT 660  
 QY 601 EGLPLRKSEHAFYLDWAVSRFTRITGQVDTQIHTHMCYCSNFNDIHSIDMDADVT 660  
 Db 61 TPSYDQVDTTAMGAVPERYSWTOGEIGSTYPSMARGNATPAMENTKWFDTNHF 120  
 QY 61 TPSYDQVDTTAMGAVPERYSWTOGEIGSTYPSMARGNATPAMENTKWFDTNHF 120  
 Db 121 VPELGPSTKPTYASHKAVSEYKEAKALGIDTVPLVGPVSYLLSKPAKGKPSLSSL 180  
 121 VPELGPNTKPSYSSHAKAVSEYKEAKALGIDTVPLVGPVSYLLSKPAKGKPSLSSL 180  
 QY 181 LGSLTPYKEVWAKAGASWIQDDEPTVNDLQHAEFLAFASSAYAELSSFSGNVNL 240  
 661 ENSRSEDEKULSVFREGVKYKGIGPGVYDHSRIPSTDIBADRINKMLAVLQNILWN 720  
 Db 181 LSSLTPYKEVWAKAGAATWQFDEPTVNDLQHAEFLAFASSAYTELESALSGNVNL 240  
 QY 241 ETYFADIPASPSYKILTSLSGVTAYGFDLIRGAKTDLRSS - FPGSKYLPGAVVGDGRNIV 299  
 Db 241 ETYFADIPASPSYKILTSLSGVTAYGFDLIRGSKTLDKLSAGSPGSKYLPGAVVGDGRNIV 300  
 QY 300 ADDLAASSTLHSLEAVAGKDKLKVSTSCSLMHTAVDVLNETKLDDETSKSWAFAAQKV 359  
 301 ADDLAASSTLHSLEAVOKDKLKVSTSCSLMHTAVDVLNETKLDSEKSWAFAAQKV 360  
 QY 360 EVNALAKALAGAQKDE-----VFAAMAAQSRSSPRVTEBEVQAA 402  
 Db 361 EVNALAKALAGAQKDEHKLKULLITYFVNINIVQYFAAMAAQSRSSPRVTEBEVQAA 420  
 QY 403 AALGSDHRRSTVSARLDAQQKLNLPVLPPTTIGSPPQTVELRVRREYKAKKITEDE 462

